

FELC COPY

A:Molecule type: protein
 A:Residues: 228-241;265-272;458-464;467-488 <MO2>
 C:Genetics:
 A:Map position: 4COP9-4G3845
 C:Function:
 A:Description: hydrolyzes 1,4-glycosidic linkages of starch, removing maltose units suc
 C:Superfamily: beta-amylase
 C:Keywords: glycosidase; hydrolase; monomer; polysaccharide degradation
 F:2-503/Product: beta-amylase #status predicted <MAT>
 F:190,384/Active site: Glu #status predicted

Query Match 35.1%; Score 1092.5; DB 1; Length 499;
 Best Local Similarity 47.5%; Pred. No. 6.9e-78;
 Matches 210; Conservative 84; Mismatches 137; Indels 11; Gaps 8;

QY 112 VPVFMPLDSVKMDHTVNRKKAMNASLOALKSAGVEGIMDMVWGLVERDAPGEYNGG 170
 DB 14 VPVYVALPGVNVNENFADPEITLQTLKKEAGVDGVMDVWVGGIIESGPKQYDWT 73
 QY 171 GYAELEMAKKGHLKQVAVMSFHQCGGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGRN 230
 DB 74 AYKTFQIARLGLKQAIMSFHRCGGNIGDDVNIPIKVVLEIGDSNPDIFYTNKSGNRN 125
 QY 231 NFEYVSLGCDTLPLVLKGRTPVQCYSDPMRGFRDFENLLG-DTIVEIQVGMGPAGELRYP 288
 DB 134 DIELYLSIGVDNLPLFAGTAVQVLYSDYMSFKENWADLLEAGVIVDIEVGLGPAGELRY 193
 QY 289 PSYPEKGVWPPGIGAFQCYDKYKIMISSLOGAEEAFKPEWGTGPTDAGQYNNWPDITN 348
 DB 194 PSYQSQG-WVPFGICEFCYDKYLRSDYEEBVRRIHGPEN-KLPENAGEVNSVPCETE 250
 QY 349 FFKKGGGWDGSGYGEFFLTWYSEMLLNHGRILQSAKAFEDKGVKISVKIAGIHHWYGT 408
 DB 251 FFKKD-CYVSEKGFNTWYNSKLIHFHGLQILGEANKIFAGLKNVLAAKVSGIHWLNH 309
 QY 409 RSHAPELTAGYNNRNDGYLPIAOMLARGAVNFTCVEMRDHEQPDQALCAPEKLVRQ 468
 DB 310 HSHAELTAGYNNLFRKDGYPARMESKYGILNFTCLEMKNTQEPAPAKAKSGPOELVQ 369
 QY 469 VALATQEAQVPLAGNALPRYDDYAHQIL--OASSLNINDQSGDRECAFTYLRMNP 525
 DB 370 VLSKAKKEGIEVAGENALETYGAKGYNQILLNAPNGVNEPKPLR-MYGTYLRISDT 428
 QY 526 LHPDNRFRVAFVKKMEKGD 547
 DB 429 VFOENNFELFKLVKMHADQD 450

RESULT 13
 C84731
 probable beta-amylase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: C84731
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PIDN:AAC69949.1; GSPDB:GN00139
 A:Accession: C84731
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-505 <STO>
 A:Cross-references: GB:A8002093; NID:g3831467; PIDN:AAC69949.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g32290
 A:Map position: 2
 C:Superfamily: beta-amylase

Query Match 35.1%; Score 1092.5; DB 2; Length 505;
 Best Local Similarity 44.4%; Pred. No. 7e-78;
 Matches 204; Conservative 89; Mismatches 155; Indels 11; Gaps 4;

QY 112 VPVFMPLDSVKMDHTVNRKKAMNASLOALKSAGVEGIMDMVWGLVERDAPGEYNGG 171
 DB 10 QVYVYMLPLDVVSDNFKFGEDEIRAQLKLLTEAGVDGVMDVWGLVSGKPKAYDWSA 69
 QY 172 YAELEMAKKGHLKQVAVMSFHQCGGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGRN 231
 DB 70 YKQVFDLVHEAGLKLQAIMSFHRCGGNIGDDVNIPIQWVRVGVGATGPTFFTNRSGNRN 129
 QY 232 FFEYVSLGCDTLPLVLKGRTPVQCYSDPMRGFRDFENLL-GDTIVEIQVGMGPAGELRYP 290
 DB 130 IEVLTGLVDQDPLFHGRGTAVQVYADYMASFRENKRFLLDAGTIVDIEVGLGPAGELRYP 189

Query Match 34.6%; Score 1079.5; DB 1; Length 503;
 Best Local Similarity 48.6%; Pred. No. 7.3e-77;
 Matches 211; Conservative 74; Mismatches 142; Indels 7; Gaps 6;

QY 112 VPVFMPLDSVKMDHTVNRKKAMNASLOALKSAGVEGIMDMVWGLVERDAPGEYNGG 171
 DB 10 QVYVYMLPLDVVSDNFKFGEDEIRAQLKLLTEAGVDGVMDVWGLVSGKPKAYDWSA 69
 QY 172 YAELEMAKKGHLKQVAVMSFHQCGGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGRN 231
 DB 70 YKQVFDLVHEAGLKLQAIMSFHRCGGNIGDDVNIPIQWVRVGVGATGPTFFTNRSGNRN 129
 QY 232 FFEYVSLGCDTLPLVLKGRTPVQCYSDPMRGFRDFENLL-GDTIVEIQVGMGPAGELRYP 290
 DB 130 IEVLTGLVDQDPLFHGRGTAVQVYADYMASFRENKRFLLDAGTIVDIEVGLGPAGELRYP 189

RESULT 14
 JQ2248
 beta-amylase (EC 3.2.1.2) - rye
 N:Alternate names: 1,4-alpha-D-glucan maltohydrolase
 C:Species: Secale cereale (rye)
 C>Date: 03-May-1994 #sequence_revision 25-Oct-1996 #text_change 28-May-1999
 C:Accession: JQ2248
 R:Sadowski, J.; Rorat, T.; Cooke, R.; Delseny, M.
 Plant Physiol. 102, 315-316, 1993
 A:Title: Nucleotide sequence of a cDNA clone encoding ubiquitous beta-amylase in rye
 A:Reference number: JQ2248; MUID:94151427; PMID:8108499
 A:Accession: JQ2248
 A:Molecule type: mRNA
 A:Residues: 1-503 <SAD>
 A:Cross-references: GB:211772; NID:g393449; PIDN:CAA77817.1; PID:g393450
 C:Function:
 A:Description: hydrolyzes 1,4-glycosidic linkages of starch, removing maltose units s
 C:Superfamily: beta-amylase
 C:Keywords: glycoprotein; glycosidase; hydrolase; monomer; polysaccharide degradation
 F:2-503/Product: beta-amylase #status predicted <MAT>
 F:184,378/Active site: Glu #status predicted
 F:249,338/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.6%; Score 1079.5; DB 1; Length 503;
 Best Local Similarity 48.6%; Pred. No. 7.3e-77;
 Matches 211; Conservative 74; Mismatches 142; Indels 7; Gaps 6;

QY 112 VPVFMPLDSVKMDHTVNRKKAMNASLOALKSAGVEGIMDMVWGLVERDAPGEYNGG 171
 DB 10 QVYVYMLPLDVVSDNFKFGEDEIRAQLKLLTEAGVDGVMDVWGLVSGKPKAYDWSA 69
 QY 172 YAELEMAKKGHLKQVAVMSFHQCGGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGRN 231
 DB 70 YKQVFDLVHEAGLKLQAIMSFHRCGGNIGDDVNIPIQWVRVGVGATGPTFFTNRSGNRN 129
 QY 232 FFEYVSLGCDTLPLVLKGRTPVQCYSDPMRGFRDFENLL-GDTIVEIQVGMGPAGELRYP 290
 DB 130 IEVLTGLVDQDPLFHGRGTAVQVYADYMASFRENKRFLLDAGTIVDIEVGLGPAGELRYP 189